

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/785,220B  
Source: 1Fw16  
Date Processed by STIC: 8/30/05

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IFW16

## RAW SEQUENCE LISTING

DATE: 08/30/2005

PATENT APPLICATION: US/10/785,220B

TIME: 08:39:24

Input Set : A:\39780-1216R1D4 SAVED AUGUST 17 2005.TXT

Output Set: N:\CRF4\08302005\J785220B.raw

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4 <110> APPLICANT: Ashkenazi, Avi J.
5      Fong, Sherman
6      Goddard, Audrey
7      Gurney, Austin L.
8      Napier, Mary A.
9      Tumas, Daniel
10     Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
13     THE TREATMENT OF DISEASES CHARACTERIZED BY A33- RELATED
14     ANTIGENS
16 <130> FILE REFERENCE: 39780-1216R1D4
18 <140> CURRENT APPLICATION NUMBER: 10/785,220B
19 <141> CURRENT FILING DATE: 2004-02-24
21 <150> PRIOR APPLICATION NUMBER: US 09/254,465
22 <151> PRIOR FILING DATE: 1999-03-05
24 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
25 <151> PRIOR FILING DATE: 1998-11-20
27 <150> PRIOR APPLICATION NUMBER: US 60/066,364
28 <151> PRIOR FILING DATE: 1997-11-21
30 <150> PRIOR APPLICATION NUMBER: US 60/078,936
31 <151> PRIOR FILING DATE: 1998-03-20
33 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
34 <151> PRIOR FILING DATE: 1998-09-17
36 <160> NUMBER OF SEQ ID NOS: 30
38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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42 <212> TYPE: PRT
43 <213> ORGANISM: Homo sapiens
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48 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
49          20          25          30
50 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
51          35          40          45
52 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
53          50          55          60
54 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
55 65          70          75          80
56 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
57          85          90          95
58 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser

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59          100          105          110
60 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
61          115          120          125
62 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
63          130          135          140
64 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
65 145          150          155          160
66 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
67          165          170          175
68 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
69          180          185          190
70 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
71          195          200          205
72 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
73          210          215          220
74 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
75 225          230          235          240
76 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
77          245          250          255
78 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
79          260          265          270
80 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
81          275          280          285
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93 1          5          10          15
94 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
95          20          25          30
96 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
97          35          40          45
98 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
99          50          55          60
100 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
101 65          70          75          80
102 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
103          85          90          95
104 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
105          100          105          110
106 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
107          115          120          125
108 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
109          130          135          140
110 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg

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111 145          150          155          160
112 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
113          165          170          175
114 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
115          180          185          190
116 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
117          195          200          205
118 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
119          210          215          220
120 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
121 225          230          235          240
122 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
123          245          250          255
124 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
125          260          265          270
126 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
127          275          280          285
128 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
129          290          295          300
130 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
131 305          310          315          320
132 Arg
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137 <211> LENGTH: 390
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Consensus DNA Sequence
144 <400> SEQUENCE: 3
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146 ttgtatggct tctgaggaag gcggcaacag ctatggggag gtcaagggtca agctcatcgt 120
147 gcttgtgcct ccattccaagc ctacagttaa catccctcc tctgccacca ttgggaaccg 180
148 ggcagtgcctg acatgctcag aacaagatgg ttccccacct tctgaataca cctgggttcaa 240
149 agatgggata gtgatgccta cgaatcccaa aagcaccctg gccttcagca actcttcccta 300
150 tgtcctgaat cccacaacag gagagctggg ctttgatccc ctgtcagcct ctgatactgg 360
151 agaatacagc tgtgaggcac ggaatgggta          390
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154 <211> LENGTH: 726
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Consensus DNA Sequence
161 <400> SEQUENCE: 4
162 tctcagtcct ctcgctgtag tcgcggagct gtgttctgtt tcccaggagt ccttcggcgg 60
163 ctgttgtgct caggtgcgcc tgatcgcat ggggacaaag gcgcaagctc gagaggaaac 120
164 tgttgtgcct ctcatattg gcgatcctgt tgtgtccct ggcattgggc agtggttacag 180
165 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
166 gcctactcgg gcttttcttc tccccgtgtg gagtgggaagt ttgaccaagg agacaccacc 300
167 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttcttg 360

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168 ccaactggta tcaccttcaa gtccgtgaca cggaagaca ctgggacata cacttgatg 420
169 gtctctgagg aaggcggcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttg 480
170 cctccatcca agcctacagt taacatcccc tcctctgcca ccattgggaa ccgggcagt 540
171 ctgacatgct cagaacaaga tggttcccca cttctgaat acacctggtt caaagatggg 600
172 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc ctatgtcctg 660
173 aatcccacaa caggagagct ggtctttgat cccctgtcag cctctgatac tggagaatac 720
174 agctgt 726
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 1503
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Consensus DNA Sequence
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186 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120
187 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
188 ctctgtctcc aagccacacag tgacaactgg cagcggttat ggcttcacgg tgccccagg 240
189 aatgaggatt agccttcaat gccagggttc ggggttctcc tcccatcagt tatatttgg 300
190 ataagcaaca gactaataac cagggaaccc atcaaagtag caaccctaag taccttactc 360
191 ttcaagcctg cggatgtagc cgactcaggc tcctatttct gcactgcaa gggccagggt 420
192 ggctctgagc agcacagcga cattgtgaag ttgtgtgca aagactctc aaagctactc 480
193 aagaccaaga ctgaggcacc tacaacctg acatacccct tgaaagcaac atctacagt 540
194 aagcagtcct gggactggac cactgacatg gatggctacc ttggagagac cagtgtggg 600
195 ccaggaaaaga gcctgcctgt ctttgccatc atcctcatca tctccttg 660
196 gtttttacca tggcctatat catgctctgt cggaagacat cccaacaaga gcatgtctac 720
197 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaacat gagggtg 780
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203 ctaccaacac tggagccgct gggagtcact ggctttgccc tgggaatttg cagatgcac 1140
204 tcaagtaagc cagctgctgg atttggtctt gggcccttct agtatctctg ccgggggctt 1200
205 ctggtactcc tctctaaata ccagaggga gatgccata gcactaggac ttggtcatca 1260
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208 cagcttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
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210 aaa 1503
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 319
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 6
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219 1 5 10 15
220 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
221 20 25 30

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222 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
223      35                      40                      45
224 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
225      50                      55                      60
226 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
227 65                      70                      75                      80
228 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
229      85                      90                      95
230 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
231      100                     105                     110
232 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
233      115                     120                     125
234 Thr Lys Ser Arg Val Arg Leu Val Leu Val Pro Pro Ser Lys Pro
235      130                     135                     140
236 Glu Cys Gly Ile Glu Gly Thr Ile Ile Gly Asn Asn Ile Gln Leu
237 145                     150                     155                     160
238 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
239      165                     170                     175
240 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
241      180                     185                     190
242 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
243      195                     200                     205
244 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
245      210                     215                     220
246 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
247 225                     230                     235                     240
248 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
249      245                     250                     255
250 Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
251      260                     265                     270
252 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
253      275                     280                     285
254 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
255      290                     295                     300
256 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
257 305                     310                     315
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261 <211> LENGTH: 2181
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 7
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268 ggggatctta ctgggcctgc tactcctggg gcacctaa ca gtggacactt atggccgtcc 180
269 catcctggaa gtgccagaga gtgtaacagg accttgga aa ggggatgtga atcttccctg 240
270 cacctatgac cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
271 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
272 gtaccagggc cgctgcatg tgagccacaa ggttcaggga gatgtatccc tccaattgag 420
273 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480

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**VERIFICATION SUMMARY**

DATE: 08/30/2005

PATENT APPLICATION: US/10/785,220B

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